RAW SEQUENCE LISTING PATENT APPLICATION US/08/482,785

DATE: 10/27/95 TIME: 09:47:56

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1	SEQUENCE LISTING	
2		51,817
3	(1) General Information:	
4		שוט ני
5	(i) APPLICANT: Adams, Craig W.	
6	Pang, Patty PY.	
7	Belei, Marina	
8		_
9	(ii) TITLE OF INVENTION: Recombinant DNase B Derived	from
10	Streptococcus pyogenes	
11		
12	(iii) NUMBER OF SEQUENCES: 16	
13		
14	(iv) CORRESPONDENCE ADDRESS:	
15	(A) ADDRESSEE: Sheldon & Mak	
16	(B) STREET: 225 South Lake Avenue, Ninth Floor	
17	(C) CITY: Pasadena	
18 19	(D) STATE: California	
20	(E) COUNTRY: USA (F) ZIP: 91001	
21	(F) LIF: 91001	
22	(v) COMPUTER READABLE FORM:	
23	(A) MEDIUM TYPE: Floppy disk	
24	(B) COMPUTER: IBM PC compatible	
25	(C) OPERATING SYSTEM: PC-DOS/MS-DOS	
26	(D) SOFTWARE: PatentIn Release #1.0, Version #	1.25
27		
28	(vi) CURRENT APPLICATION DATA:	
29	(A) APPLICATION NUMBER: US 08/482,785	
30	(B) FILING DATE: 07-JUN-1995	
31	(C) CLASSIFICATION: 435	
32		
33	(vii) PRIOR APPLICATION DATA:	
34	(A) APPLICATION NUMBER: US/08/393,889	
35	(B) FILING DATE: 24-FEB-1995	
36		
37	(A) APPLICATION NUMBER: US/08/082,845	
38	(B) FILING DATE:	
39		
40	(viii) ATTORNEY/AGENT INFORMATION:	
41	(A) NAME: Farber, Michael B.	
42	(B) REGISTRATION NUMBER: 32,612	
43 44	(C) REFERENCE/DOCKET NUMBER: 9521	
4.4 4.5	(iv) TELECOMMINICATION INTODUMETON.	
45 46	(ix) TELECOMMUNICATION INFORMATION:	
40	(A) TELEPHONE: (818) 796-4000	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/482,785

DATE: 10/27/95 TIME: 09:48:00

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		INPUT SET: 50937.n
47 48		(B) TELEFAX: (818) 795-6321
49		
50 51	(2) INFO	RMATION FOR SEQ ID NO:1:
52	(i)	SEQUENCE CHARACTERISTICS:
53		(A) LENGTH: 43 amino acids
54		(B) TYPE: amino acid
55		(D) TOPOLOGY: linear
56 57	(11)	MOLECULE TYPE: peptide
58	(11)	MODECOLE TIPE: peptide
59 60	(iii)	HYPOTHETICAL: NO
61	(V)	FRAGMENT TYPE: N-terminal
62	(' '	THE STATE OF THE S
63	(vi)	ORIGINAL SOURCE:
64	, ,	(A) ORGANISM: Streptococcus pyogenes
65		
66		
67 68	(X1)	SEQUENCE DESCRIPTION: SEQ ID NO:1:
68 69	Wet	Asn Leu Leu Gly Ser Arg Arg Val Phe Ser Lys Lys Cys Arg Leu
70	1	5 10 15
71	-	
72		
73	Val	Lys Phe Ser Met Val Ala Leu Val Ser Ala Thr Met Ala Val Thr
74		20 25 30
75		
76 77	mb w	Upl mbm row Clarker mbm ble row ble box
7 <i>7</i>	THE	Val Thr Leu Glu Asn Thr Ala Leu Ala Arg 35 40
70 79		33
80	(2) INFO	RMATION FOR SEQ ID NO:2:
81		
82	(i)	SEQUENCE CHARACTERISTICS:
83		(A) LENGTH: 41 base pairs
84		(B) TYPE: nucleic acid
85 86		(C) STRANDEDNESS: single (D) TOPOLOGY: linear
87		(b) TOPOLOGI: Timedi
88	(ii)	MOLECULE TYPE: DNA (genomic)
89	(/	
90	(iii)	HYPOTHETICAL: NO
91		
92	(iv)	ANTI-SENSE: NO
93		ORIGINAL GOURGE
94 95	(V1)	ORIGINAL SOURCE: (A) ORGANISM: Synthetic DNA primer
96		(A) OKOANISM: SYNCHECIC DNA PLIMEL
97		
98	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:2:
99	, ,	-

RAW SEQUENCE LISTING PATENT APPLICATION US/08/482,785

DATE: 10/27/95 TIME: 09:48:05

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		.,,
100 101	TAACGGATCC GAATCTACTT GGATCAAGAC GGGTTTTTTC T 41	
102 103	(2) INFORMATION FOR SEQ ID NO:3:	
104 105 106 107 108 109	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
110 111	(ii) MOLECULE TYPE: DNA (genomic)	
112 113	(iii) HYPOTHETICAL: NO	
114 115	(iv) ANTI-SENSE: NO	
116 117 118 119	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Synthetic DNA primer</pre>	
120 121	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
122 123	CCGGGTCGAC CCGGGGAATG ACGGCAATCA TTGCTTTTTC T 41	
124 125	(2) INFORMATION FOR SEQ ID NO:4:	
126 127 128 129 130	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
131 132	(ii) MOLECULE TYPE: peptide	
133 134	(iii) HYPOTHETICAL: NO	
135 136	(v) FRAGMENT TYPE: N-terminal	
137 138 139 140	<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Streptococcus pyogenes</pre>	
141 142	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
143 144 145 146	Gln Thr Gln Val Ser Asn Asp Val Val Leu Asn Asp Gly Ala Ser Xaa 1 5 10 15	
147 148 149	Tyr Leu Asn Glu Ala Leu Ala 20	
150 151	(2) INFORMATION FOR SEQ ID NO:5:	
152	(i) SEQUENCE CHARACTERISTICS:	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/482,785

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DATE: 10/27/95

						INI	PUT S	ET: S	6937.raw
153	(A) LENGTH: 22 base pairs	.					015	L 1. 5	0,0,1,4,1
154	(B) TYPE: nucleic acid								
155	(C) STRANDEDNESS: single								
156	(D) TOPOLOGY: linear								
157	(2) 10102011 22.001								
158	(ii) MOLECULE TYPE: DNA (genomi	c)							
159	(11) Mondoodd IIId. DAR (genomi	٠,							
160	(iii) HYPOTHETICAL: NO								
161	(III) MIIOMBIIONE. NO								
162	(iv) ANTI-SENSE: NO								
163	(17) Mill bhibh. No								
164	(vi) ORIGINAL SOURCE:								
165	(A) ORGANISM: Synthetic p	robe							
166	(II) OKOMIDII DYNCHOLIC P	1000							
167									
168	(xi) SEQUENCE DESCRIPTION: SEQ	TD NO	. 5 .						
169	(NI) Digonnon Dibonii IIon. Dig	10 110	• • •						
170	CAUACNCART NWSNAAYGAY GT				2	22			
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172									
173	(2) INFORMATION FOR SEQ ID NO:6:								
174	(2) Intomuniton ton bly 15 note.								
175	(i) SEQUENCE CHARACTERISTICS:								
176	(A) LENGTH: 38 amino acid	s							
177	(B) TYPE: amino acid	_							
178	(D) TOPOLOGY: linear								
179	(b) Torodoor. Ifficar								
180	(ii) MOLECULE TYPE: peptide								
181	(11) Hollool IIII Popular								
182	(iii) HYPOTHETICAL: NO								
183	(,								
184	(v) FRAGMENT TYPE: N-terminal								
185	(, , , , , , , , , , , , , , , , , , ,								
186	(vi) ORIGINAL SOURCE:								
187	(A) ORGANISM: Streptococc	us pvo	ogene	es					
188	(,	F7							
189									
190									
191	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO	:6:						
192	(, <u>-</u>								
193	Arg Gln Thr Gln Val Ser Asn As	p Val	Val	Leu	Asn	Asp	Glv	Ala	Ser
194	1 5	-	10				- 2	15	
195									
196									
197	Lys Tyr Leu Asn Glu Ala Leu Al	a Trp	Thr	Phe	Asn	Asp	Ser	Pro	Asn
198	20	25					30		
199							-		
200									
201	Tyr Tyr Lys Thr Leu Gly								
202	35								
203									
204	(2) INFORMATION FOR SEQ ID NO:7:								
205									

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208 209		•	•	YPE:												
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210		(1)) T	OPOLO	JGY:	Tine	ear									
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212	(11) MOI	-ECOI	-E T	(PE:	DNA	(ge	nomi	C)							
213	/ 4 4 4	\ 1337) (mi ii	am T (1)		170										
214	(111) HYE	OTH	STIC	4T: 1	NO										
216	/	\	OT 01	ance.	NO.											
217	(10) ANT	11-21	- NOE	: NO											
217	(***) ORI	COTNI	AT C	MIDGI											
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223		•	•	CAT			94	A								
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225																
226	/vi) SEC	אווראנ	וח שי	יפרם:	דייים	าพ •	SEO .	TD NO	1.7.						
227	/ 77	, 55,	SORM	וט טו	JOCK.	1111	J14	JEQ.	ID IN	<i>J</i> . , .						
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2.3.1																
231 232	ACAAGCA	ጥ ልጥር	TAA E	г ста	A CITY	r gg	а тел	A AG	A CGG	יידים כ	ր արարո	י יייטיי	מ ב יו	Δ Δ Δ Δ	ስ ጥርጥ	170
232	ACAAGCA															170
232 233	ACAAGCA	Met	t Asr			ı Gly	y Se				l Phe	e Se			A TGT s Cys	170
232 233 234	ACAAGCA	Met				ı Gly						e Se				170
232 233		Met 1	t Asr l	n Lei	ı Let	ı Gl	y Sei	r Ar	g Ar	g Va	l Phe	e Se:	r Ly:	s Ly:	s Cys	
232 233 234 235	CGG CTA	Met I GTA	t Asr l AAA	n Leu TTT	ı Let TCA	J Gl	y Sei 5 GTA	r Arg	g Arg	g Vai	l Phe le TCA	e Sei O GCC	r Ly: ACA	s Ly:	s Cys GCT	170 218
232 233 234 235 236		Met I GTA	t Asr l AAA	n Leu TTT	Let TCA Ser	J Gl	y Sei 5 GTA	r Arg	g Arg	g Va GTA Val	l Phe le TCA	e Sei O GCC	r Ly: ACA	s Ly:	s Cys GCT Ala	
232 233 234 235 236 237	CGG CTA Arg Leu	Met I GTA	t Asr l AAA	n Leu TTT	ı Let TCA	J Gl	y Sei 5 GTA	r Arg	g Arg	g Vai	l Phe le TCA	e Sei O GCC	r Ly: ACA	s Ly:	s Cys GCT	
232 233 234 235 236 237 238	CGG CTA Arg Leu 15	Met I GTA Val	t Asr l AAA Lys	n Lei TTT Phe	TCA Ser 20	ATG Met	y Ser GTA Val	GCT Ala	g Arg CTT Leu	g Va GTA Val 25	l Phe 10 TCA Ser	e Ser O GCC Ala	r Ly: ACA Thr	s Ly: ATG Met	GCT Ala 30	218
232 233 234 235 236 237 238 239	CGG CTA Arg Leu 15	Met GTA Val	AAA Lys GTC	TTT Phe	TCA Ser 20	ATG Met	y Ser GTA Val	GCT Ala	CTT Leu GCA	GTA Val 25	TCA Ser	GCC Ala	ACA Thr	ATG Met ACA	GCT Ala 30	
232 233 234 235 236 237 238 239 240	CGG CTA Arg Leu 15	Met GTA Val	AAA Lys GTC	TTT Phe	TCA Ser 20	ATG Met	y Ser GTA Val	GCT Ala	CTT Leu GCA	GTA Val 25	TCA Ser	GCC Ala	ACA Thr	ATG Met ACA	GCT Ala 30	218
232 233 234 235 236 237 238 239 240 241	CGG CTA Arg Leu 15	Met GTA Val	AAA Lys GTC	TTT Phe ACA Thr	TCA Ser 20	ATG Met	y Ser GTA Val	GCT Ala	CTT Leu GCA Ala	GTA Val 25	TCA Ser	GCC Ala	ACA Thr	ATG Met ACA Thr	GCT Ala 30	218
232 233 234 235 236 237 238 239 240 241 242	CGG CTA Arg Leu 15	Met GTA Val ACA Thr	AAA Lys GTC Val	TTT Phe ACA Thr 35	TCA Ser 20 CTT Leu	ATG Met GAA Glu	y Ser GTA Val AAT Asn	GCT Ala ACT Thr	CTT Leu GCA Ala 40	GTA Val 25 CTG Leu	TCA Ser GCA	GCC Ala CGA Arg	ACA Thr CAA	ATG Met ACA Thr	GCT Ala 30 CAG Gln	218
232 233 234 235 236 237 238 239 240 241 242 243	CGG CTA Arg Leu 15 GTA ACA Val Thr	Met I GTA Val ACA Thr	AAA Lys GTC Val	TTT Phe ACA Thr 35	TCA Ser 20 CTT Leu	ATG Met GAA Glu	y Ser GTA Val AAT ASN	GCT Ala ACT Thr	CTT Leu GCA Ala 40	GTA Val 25 CTG Leu	TCA Ser GCA Ala	GCC Ala CGA Arg	ACA Thr CAA Gln	ATG Met ACA Thr 45	GCT Ala 30 CAG Gln	218
232 233 234 235 236 237 238 239 240 241 242 243 244	CGG CTA Arg Leu 15 GTA ACA Val Thr	Met I GTA Val ACA Thr	AAA Lys GTC Val	TTT Phe ACA Thr 35	TCA Ser 20 CTT Leu	ATG Met GAA Glu	y Ser GTA Val AAT ASN	GCT Ala ACT Thr	CTT Leu GCA Ala 40	GTA Val 25 CTG Leu	TCA Ser GCA Ala	GCC Ala CGA Arg	ACA Thr CAA Gln	ATG Met ACA Thr 45	GCT Ala 30 CAG Gln	218
232 233 234 235 236 237 238 239 240 241 242 243 244 245	CGG CTA Arg Leu 15 GTA ACA Val Thr	Met I GTA Val ACA Thr	AAA Lys GTC Val GAT Asp	TTT Phe ACA Thr 35	TCA Ser 20 CTT Leu	ATG Met GAA Glu	y Ser GTA Val AAT ASN	GCT Ala ACT Thr	CTT Leu GCA Ala 40	GTA Val 25 CTG Leu	TCA Ser GCA Ala	GCC Ala CGA Arg	ACA Thr CAA Gln TAC Tyr	ATG Met ACA Thr 45	GCT Ala 30 CAG Gln	218
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser	GTA Val ACA Thr	AAA Lys GTC Val GAT Asp	TTT Phe ACA Thr 35 GTT Val	TCA Ser 20 CTT Leu GTT Val	ATG Met GAA Glu CTA Leu	GTA Val AAT ASN	GCT Ala ACT Thr GAT Asp	CTT Leu GCA Ala 40 GGC Gly	GTA Val 25 CTG Leu GCA	TCA Ser GCA Ala AGC Ser	GCC Ala CGA Arg	ACA Thr CAA Gln TAC Tyr 60	ATG Met ACA Thr 45 CTA Leu	GCT Ala 30 CAG Gln AAC Asn	218
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser GAA GCA	GTA Val ACA Thr AAT ASN	AAA Lys GTC Val GAT Asp 50	TTT Phe ACA Thr 35 GTT Val	TCA Ser 20 CTT Leu GTT Val	ATG Met GAA Glu CTA Leu	GTA Val AAT ASN AAT ASN	GCT Ala ACT Thr GAT Asp 55	CTT Leu GCA Ala 40 GGC Gly	GTA Val 25 CTG Leu GCA Ala	TCA Ser GCA Ala AGC Ser	GCC Ala CGA Arg AAG Lys	ACA Thr CAA Gln TAC Tyr 60	ATG Met ACA Thr 45 CTA Leu	GCT Ala 30 CAG Gln AAC Asn	218 266 314
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser	GTA Val ACA Thr AAT ASN	AAA Lys GTC Val GAT Asp 50	TTT Phe ACA Thr 35 GTT Val	TCA Ser 20 CTT Leu GTT Val	ATG Met GAA Glu CTA Leu	GTA Val AAT ASN AAT ASN	GCT Ala ACT Thr GAT Asp 55	CTT Leu GCA Ala 40 GGC Gly	GTA Val 25 CTG Leu GCA Ala	TCA Ser GCA Ala AGC Ser	GCC Ala CGA Arg AAG Lys	ACA Thr CAA Gln TAC Tyr 60	ATG Met ACA Thr 45 CTA Leu	GCT Ala 30 CAG Gln AAC Asn	218 266 314
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser GAA GCA	GTA Val ACA Thr AAT Asn TTA Leu	AAA Lys GTC Val GAT Asp 50	TTT Phe ACA Thr 35 GTT Val	TCA Ser 20 CTT Leu GTT Val	ATG Met GAA Glu CTA Leu	GTA Val AAT ASN AAT ASN	GCT Ala ACT Thr GAT Asp 55	CTT Leu GCA Ala 40 GGC Gly	GTA Val 25 CTG Leu GCA Ala	TCA Ser GCA Ala AGC Ser	GCC Ala CGA Arg AAG Lys TAT	ACA Thr CAA Gln TAC Tyr 60	ATG Met ACA Thr 45 CTA Leu	GCT Ala 30 CAG Gln AAC Asn	218 266 314
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser GAA GCA	GTA Val ACA Thr AAT Asn TTA Leu 65	AAA Lys GTC Val GAT Asp 50 GCT	TTT Phe ACA Thr 35 GTT Val	TCA Ser 20 CTT Leu GTT Val	ATG Met GAA Glu CTA Leu TTC Phe	GTA Val AAT ASN AAT ASN AAT ASN	GCT Ala ACT Thr GAT Asp 55 GAC Asp	CTT Leu GCA Ala 40 GGC Gly AGT Ser	GTA Val 25 CTG Leu GCA Ala	TCA Ser GCA Ala AGC Ser AAC	GCC Ala CGA Arg AAG Lys TAT Tyr 75	ACA Thr CAA Gln TAC Tyr 60 TAC	ATG Met ACA Thr 45 CTA Leu	GCT Ala 30 CAG Gln AAC Asn ACT Thr	218 266 314
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser GAA GCA Glu Ala	GTA Val ACA Thr AAT Asn TTA Leu 65	AAA Lys GTC Val GAT Asp 50 GCT Ala	TTT Phe ACA Thr 35 GTT Val TGG Trp	TCA Ser 20 CTT Leu GTT Val ACA Thr	ATG Met GAA Glu CTA Leu TTC Phe	GTA Val AAT ASN AAT ASN AAT CCA	GCT Ala ACT Thr GAT Asp 55 GAC Asp	CTT Leu GCA Ala 40 GGC Gly AGT Ser	GTA Val 25 CTG Leu GCA Ala CCT Pro	TCA Ser GCA Ala AGC Ser AAC ASn	GCC Ala CGA Arg AAG Lys TAT Tyr 75	ACA Thr CAA Gln TAC Tyr 60 TAC Tyr	ATG Met ACA Thr 45 CTA Leu AAA Lys	GCT Ala 30 CAG Gln AAC Asn ACT Thr	218 266 314 362
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser GAA GCA Glu Ala	GTA Val ACA Thr AAT Asn TTA Leu 65	AAA Lys GTC Val GAT Asp 50 GCT Ala	TTT Phe ACA Thr 35 GTT Val TGG Trp	TCA Ser 20 CTT Leu GTT Val ACA Thr	ATG Met GAA Glu CTA Leu TTC Phe	GTA Val AAT ASN AAT ASN AAT CCA	GCT Ala ACT Thr GAT Asp 55 GAC Asp	CTT Leu GCA Ala 40 GGC Gly AGT Ser	GTA Val 25 CTG Leu GCA Ala CCT Pro	TCA Ser GCA Ala AGC Ser AAC ASn	GCC Ala CGA Arg AAG Lys TAT Tyr 75	ACA Thr CAA Gln TAC Tyr 60 TAC Tyr	ATG Met ACA Thr 45 CTA Leu AAA Lys	GCT Ala 30 CAG Gln AAC Asn ACT Thr	218 266 314 362
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser GAA GCA Glu Ala TTA GGT Leu Gly	GTA Val ACA Thr AAT Asn TTA Leu 65	AAA Lys GTC Val GAT Asp 50 GCT Ala	TTT Phe ACA Thr 35 GTT Val TGG Trp	TCA Ser 20 CTT Leu GTT Val ACA Thr	ATG Met GAA Glu CTA Leu TTC Phe ACT Thr	GTA Val AAT ASN AAT ASN AAT CCA	GCT Ala ACT Thr GAT Asp 55 GAC Asp	CTT Leu GCA Ala 40 GGC Gly AGT Ser	GTA Val 25 CTG Leu GCA Ala CCT Pro	TCA Ser GCA Ala AGC Ser AAC ASn	GCC Ala CGA Arg AAG Lys TAT Tyr 75	ACA Thr CAA Gln TAC Tyr 60 TAC Tyr	ATG Met ACA Thr 45 CTA Leu AAA Lys	GCT Ala 30 CAG Gln AAC Asn ACT Thr	218 266 314 362
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser GAA GCA Glu Ala TTA GGT Leu Gly 80 ATT CTC	GTA Val ACA Thr AAT Asn TTA Leu 65 ACT Thr	AAA Lys GTC Val GAT Asp 50 GCT Ala AGT Ser	TTT Phe ACA Thr 35 GTT Val TGG Trp CAG Gln	TCA Ser 20 CTT Leu GTT Val ACA Thr	ATG Met GAA Glu CTA Leu TTC Phe ACT Thr 85	GTA Val AAT Asn AAT Asn CCA Pro	GCT Ala ACT Thr GAT Asp 55 GAC Asp GCA Ala	CTT Leu GCA Ala 40 GGC Gly AGT Ser CTC Leu	GTA Val 25 CTG Leu GCA Ala CCT Pro TTT Phe	TCA Ser GCA Ala AGC Ser AAC ASn CCT Pro 90 ACG	GCC Ala CGA Arg AAG Lys TAT Tyr 75 AAA Lys	ACA Thr CAA Gln TAC Tyr 60 TAC Tyr GCA Ala	ATG Met ACA Thr 45 CTA Leu AAA Lys GGA Gly	GCT Ala 30 CAG Gln AAC Asn ACT Thr GAT Asp	218 266 314 362
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 256 257	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser GAA GCA Glu Ala TTA GGT Leu Gly 80	GTA Val ACA Thr AAT Asn TTA Leu 65 ACT Thr	AAA Lys GTC Val GAT Asp 50 GCT Ala AGT Ser	TTT Phe ACA Thr 35 GTT Val TGG Trp CAG Gln	TCA Ser 20 CTT Leu GTT Val ACA Thr	ATG Met GAA Glu CTA Leu TTC Phe ACT Thr 85	GTA Val AAT Asn AAT Asn CCA Pro	GCT Ala ACT Thr GAT Asp 55 GAC Asp GCA Ala	CTT Leu GCA Ala 40 GGC Gly AGT Ser CTC Leu	GTA Val 25 CTG Leu GCA Ala CCT Pro TTT Phe	TCA Ser GCA Ala AGC Ser AAC ASn CCT Pro 90 ACG	GCC Ala CGA Arg AAG Lys TAT Tyr 75 AAA Lys	ACA Thr CAA Gln TAC Tyr 60 TAC Tyr GCA Ala	ATG Met ACA Thr 45 CTA Leu AAA Lys GGA Gly	GCT Ala 30 CAG Gln AAC Asn ACT Thr GAT Asp	218 266 314 362 410
232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 256	CGG CTA Arg Leu 15 GTA ACA Val Thr GTC TCA Val Ser GAA GCA Glu Ala TTA GGT Leu Gly 80 ATT CTC	GTA Val ACA Thr AAT Asn TTA Leu 65 ACT Thr	AAA Lys GTC Val GAT Asp 50 GCT Ala AGT Ser	TTT Phe ACA Thr 35 GTT Val TGG Trp CAG Gln	TCA Ser 20 CTT Leu GTT Val ACA Thr	ATG Met GAA Glu CTA Leu TTC Phe ACT Thr 85	GTA Val AAT Asn AAT Asn CCA Pro	GCT Ala ACT Thr GAT Asp 55 GAC Asp GCA Ala	CTT Leu GCA Ala 40 GGC Gly AGT Ser CTC Leu	GTA Val 25 CTG Leu GCA Ala CCT Pro TTT Phe	TCA Ser GCA Ala AGC Ser AAC ASn CCT Pro 90 ACG	GCC Ala CGA Arg AAG Lys TAT Tyr 75 AAA Lys	ACA Thr CAA Gln TAC Tyr 60 TAC Tyr GCA Ala	ACA Thr 45 CTA Leu AAA Clys GGA Gly	GCT Ala 30 CAG Gln AAC Asn ACT Thr GAT Asp	218 266 314 362 410

SEQUENCE VERIFICATION REPORT PATENT APPLICATION *US/08/482,785*

DATE: 10/27/95 TIME: 09:48:17

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Original Text